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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/537,654

DATE: 04/18/2000
TIME: 17:44:21

Input Set: I537654.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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TECH CENTER 1600/2900

1 <110> APPLICANT: Mahajan, Pramod B.
2 Shi, Jinrui
3 <120> TITLE OF INVENTION: A Novel Maize Rad51-Like Gene and Uses
4 Thereof
5 <130> FILE REFERENCE: 1107
6 <140> CURRENT APPLICATION NUMBER: US/09/537,654
7 <141> CURRENT FILING DATE: 2000-03-29
8 <150> EARLIER APPLICATION NUMBER: 60/132,582
9 <151> EARLIER FILING DATE: 1999-05-05
10 <160> NUMBER OF SEQ ID NOS: 8
11 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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15 <213> ORGANISM: Zea mays
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22 cctaagcgac agcggcggcg tcgacgtaag cggtgcgtg gcgccaccga cggaggctac 180
23 gageggttgt ggaggcagat atgagaggtg gaggtggcta caacgggtcg gcggctgtga 240
24 gatactgaaa tccgcactgc agttctcttc tcccccaat cagtaccacc tctccaagtg 300
25 gcaatcacc atg gga gat caa tct ggc tct aga aat gga cca caa cag aag 351
26 Met Gly Asp Gln Ser Gly Ser Arg Asn Gly Pro Gln Gln Lys
27 1 5 10
28 tac gtt tca gga gcc cag aat gcc tgg gat atg ttc tct gat gag ctg 399
29 Tyr Val Ser Gly Ala Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu
30 15 20 25 30
31 tca cag aaa cac atc act act ggt tct ggt gac ctc aat gac ata ctt 447
32 Ser Gln Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu
33 35 40 45
34 ggt ggc ggg att cac tgc aaa gaa gtt act gag atc ggt ggc gtc cca 495
35 Gly Gly Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro
36 50 55 60
37 ggg gtt ggt aaa act caa ctg ggg att caa cta gca atc aat gta caa 543
38 Gly Val Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln
39 65 70 75
40 atc cca gtg gaa tgt ggt ggc ctt ggt ggg aaa gca gtt tat ata gat 591
41 Ile Pro Val Glu Cys Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Asp
42 80 85 90
43 aca gag ggc agt ttc atg gtt gaa cgt gtc tac cag att gct gaa ggg 639
44 Thr Glu Gly Ser Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly

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45	95	100	105	110	
46	tgt att agg gac ata ctg gag cac ttt ccg cac agc cat gag aag tcc	687			
47	Cys Ile Arg Asp Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser				
48	115	120	125		
49	tct tct gtc caa aaa caa tta cag cct gag cgt ttc ctg gcg gat atc	735			
50	Ser Ser Val Gln Lys Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile				
51	130	135	140		
52	tat tac ttc cgg ata tgc agt tac acc gaa caa att gca gtc ata aac	783			
53	Tyr Tyr Phe Arg Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn				
54	145	150	155		
55	tac atg gag aag ttc ctc aga gag cat aaa gat gtg cgt ata gtt att	831			
56	Tyr Met Glu Lys Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile				
57	160	165	170		
58	att gat agt gtt act ttc cac ttt cga caa gat ttt gaa gat ctg gca	879			
59	Ile Asp Ser Val Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala				
60	175	180	185	190	
61	ctg agg acc aga gtg cta agt gga tta tca ttg aag tta atg aag att	927			
62	Leu Arg Thr Arg Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile				
63	195	200	205		
64	gca aag aca tat aac ttg gca gtt gtc ttg ttg aac caa gtc act act	975			
65	Ala Lys Thr Tyr Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr				
66	210	215	220		
67	aaa ttt aca gaa ggg tca ttt caa ttg act ctt gct cta ggt gac agc	1023			
68	Lys Phe Thr Glu Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser				
69	225	230	235		
70	tgg tcc cac tca tgc acg aac cgg ttg att ctg cac tgg aat ggg aac	1071			
71	Trp Ser His Ser Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn				
72	240	245	250		
73	gaa cga tac gca cat ctt gat aag tct cct tca ctt cca gta gcc tca	1119			
74	Glu Arg Tyr Ala His Leu Asp Lys Ser Pro Ser Leu Pro Val Ala Ser				
75	255	260	265	270	
76	gca ccg tat gca gtg aca ggc aaa ggg att aga gat gct gtg agc tca	1167			
77	Ala Pro Tyr Ala Val Thr Gly Lys Gly Ile Arg Asp Ala Val Ser Ser				
78	275	280	285		
79	aac cac aag cga gcc cga gta acg t agcattcttg gtgtcaagca	1212			
80	Asn His Lys Arg Ala Arg Val Thr				
81	290				
82	cttgtatgtc cactacgctc ctgcagcttt cttcgccatg gatcttttgg actagtgagg	1272			
83	tgagactgga gaatagtacc attttgttga ttctcagttg ctttgtgccg ttggctacca	1332			
84	accaacctta agagagaagt aaatacaaca gaacaggcta atatagtgtt ttgtatctga	1392			
85	acatctggcc catcgtacat tcagtaaagc ctataaatagc gggcaaaaaa aaaaaaaaaa	1452			
86	aaaaaaaaaa aaaaaaaaaa aa	1474			
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88	<211> LENGTH: 294				
89	<212> TYPE: PRT				
90	<213> ORGANISM: Zea mays				
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93	1 5 10 15				
94	Ser Gly Ala Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu Ser Gln				

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95          20          25          30
96  Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly
97          35          40          45
98  Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val
99          50          55          60
100 Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro
101          65          70          75          80
102 Val Glu Cys Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Asp Thr Glu
103          85          90          95
104 Gly Ser Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile
105          100          105          110
106 Arg Asp Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Ser
107          115          120          125
108 Val Gln Lys Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr
109          130          135          140
110 Phe Arg Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met
111          145          150          155          160
112 Glu Lys Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp
113          165          170          175
114 Ser Val Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg
115          180          185          190
116 Thr Arg Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys
117          195          200          205
118 Thr Tyr Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe
119          210          215          220
120 Thr Glu Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser
121          225          230          235          240
122 His Ser Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg
123          245          250          255
124 Tyr Ala His Leu Asp Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro
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126 Tyr Ala Val Thr Gly Lys Gly Ile Arg Asp Ala Val Ser Ser Asn His
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139  tgagaggttg aggtggctac aacgggtcgg cggtgtgag atactgaaat ccgcactgca
140  gttctcttct tcccccaatc agtaccacct ctccaagtgg caatcacc atg gga gat
141                                     Met Gly Asp
142                                     1
143  caa tct ggc tct aga aat gga cca caa cag aag tac gtt tca gga gcc
144  Gln Ser Gly Ser Arg Asn Gly Pro Gln Gln Lys Tyr Val Ser Gly Ala

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145	5	10	15		
146	cag aat gcc tgg gat atg ttc tct gat gag ctg tca cag aaa cac atc			273	
147	Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu Ser Gln Lys His Ile				
148	20	25	30	35	
149	act act ggt tct ggt gac ctc aat gac ata ctt ggt ggc ggg att cac			321	
150	Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly Gly Ile His				
151		40	45	50	
152	tgc aaa gaa gtt act gag atc ggt ggc gtc cca ggg gtt ggt aaa act			369	
153	Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val Gly Lys Thr				
154		55	60	65	
155	caa ctg ggg att caa cta gca atc aat gta caa atc cca gtg gaa tgt			417	
156	Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro Val Glu Cys				
157		70	75	80	
158	ggt ggc ctt ggt ggg aaa gca gtt tat ata gag ggc agt ttc atg gtt			465	
159	Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Glu Gly Ser Phe Met Val				
160		85	90	95	
161	gaa cgt gtc tac cag att gct gaa ggg tgt att agg gac ata ctg gag			513	
162	Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile Arg Asp Ile Leu Glu				
163		100	105	110	115
164	cac ttt ccg cac agc cat gag aag tcc tct tct gtc caa aaa caa tta			561	
165	His Phe Pro His Ser His Glu Lys Ser Ser Ser Val Gln Lys Gln Leu				
166		120	125	130	
167	cag cct gag cgt ttc ctg gcg gat atc tat tac ttc cgg ata tgc agt			609	
168	Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr Phe Arg Ile Cys Ser				
169		135	140	145	
170	tac acc gaa caa att gca gtc ata aac tac atg gag aag ttc ctc aga			657	
171	Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met Glu Lys Phe Leu Arg				
172		150	155	160	
173	gag cat aaa gat gtg cgt ata gtt att att gat agt gtt act ttc cac			705	
174	Glu His Lys Asp Val Arg Ile Val Ile Ile Asp Ser Val Thr Phe His				
175		165	170	175	
176	ttt cga caa gat ttt gaa gat ctg gca ctg agg acc aga gtg cta agt			753	
177	Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg Thr Arg Val Leu Ser				
178		180	185	190	195
179	gga tta tca ttg aag tta atg aag att gca aag aca tat aac ttg gca			801	
180	Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys Thr Tyr Asn Leu Ala				
181		200	205	210	
182	gtt gtc ttg ttg aac caa gtc act act aaa ttt aca gaa ggg tca ttt			849	
183	Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe Thr Glu Gly Ser Phe				
184		215	220	225	
185	caa ttg act ctt gct cta ggt gac agc tgg tcc cac tca tgc acg aac			897	
186	Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser His Ser Cys Thr Asn				
187		230	235	240	
188	cgg ttg att ctg cac tgg aat ggg aac gaa cga tac gca cat ctt gat			945	
189	Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg Tyr Ala His Leu Asp				
190		245	250	255	
191	aag tct cct tca ctt cca gta gcc tca gcc ccg tat gca gtg aca ggc			993	
192	Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro Tyr Ala Val Thr Gly				
193		260	265	270	275
194	aaa ggg att aga gat gtg tgagctcaaa ccacaagcga gcccgagtaa			1041	

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198      atggatcttt tggactagtg aggtgagact ggagaatagt accatttgat tctcagttgc      1161
199      tttgtgccgt tggctaccaa ccaaccttaa gagagaagta aatacaacag aacaggctaa      1221
200      tatagtgttt tgtatctgaa catctggccc atcgtacatt cagtaaagcc tataatagcg      1281
201      ggcatatatg tgcttctctg atcaccgatc agcaaaaaaa aaaaaaaaaa aaaaaaaaaa      1341
202      aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1401
203      aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1459
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207      <213> ORGANISM: Zea mays
208      <400> SEQUENCE: 4
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212      20                      25                      30
213      Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly
214      35                      40                      45
215      Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val
216      50                      55                      60
217      Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro
218      65                      70                      75                      80
219      Val Glu Cys Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Glu Gly Ser
220      85                      90                      95
221      Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile Arg Asp
222      100                     105                     110
223      Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Ser Val Gln
224      115                     120                     125
225      Lys Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr Phe Arg
226      130                     135                     140
227      Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met Glu Lys
228      145                     150                     155                     160
229      Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp Ser Val
230      165                     170                     175
231      Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg Thr Arg
232      180                     185                     190
233      Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys Thr Tyr
234      195                     200                     205
235      Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe Thr Glu
236      210                     215                     220
237      Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser His Ser
238      225                     230                     235                     240
239      Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg Tyr Ala
240      245                     250                     255
241      His Leu Asp Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro Tyr Ala
242      260                     265                     270
243      Val Thr Gly Lys Gly Ile Arg Asp Val
244      275                     280

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/537,654

DATE: 04/18/2000
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Input Set: I537654.RAW

Line ? Error/Warning

Original Text

314 W Invalid/Missing Amino Acid Numbering